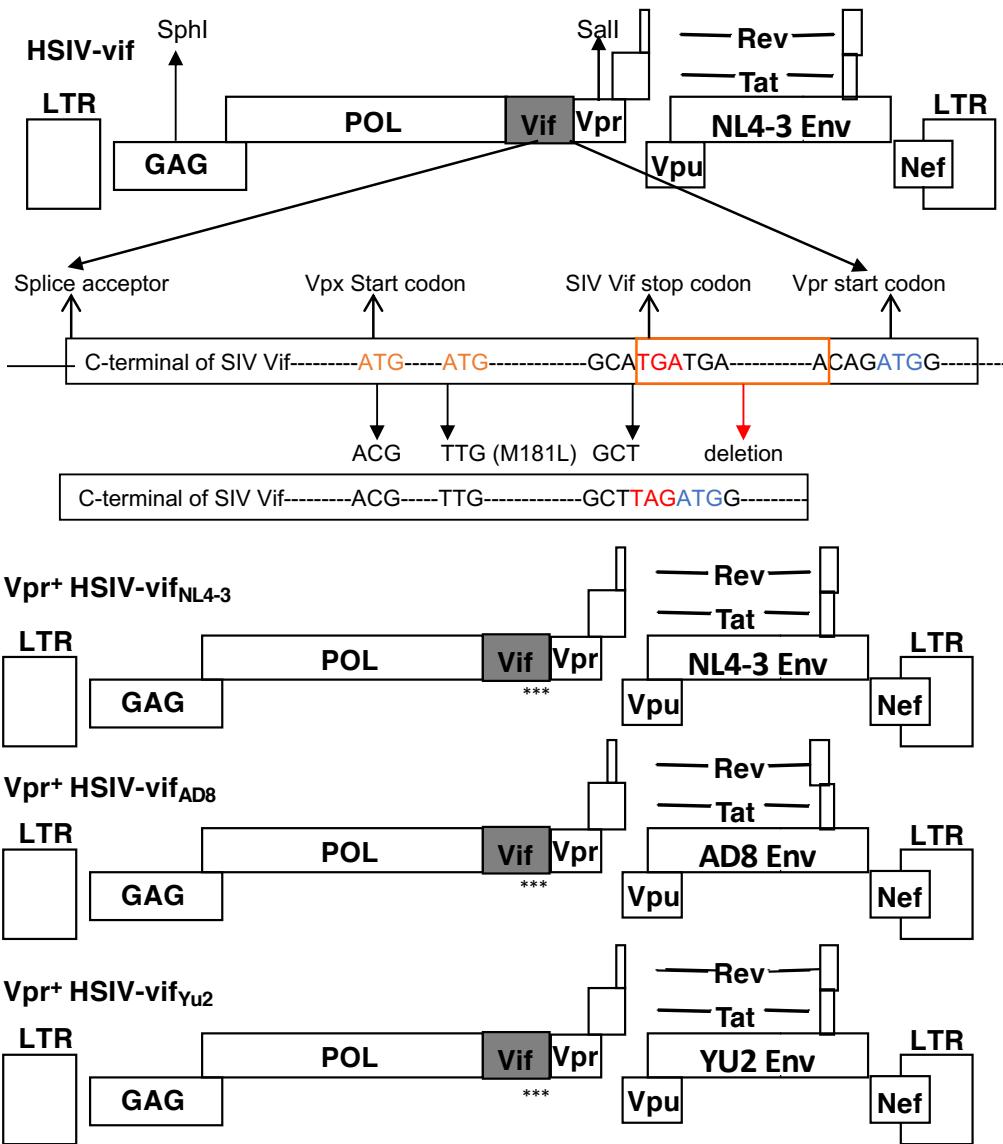
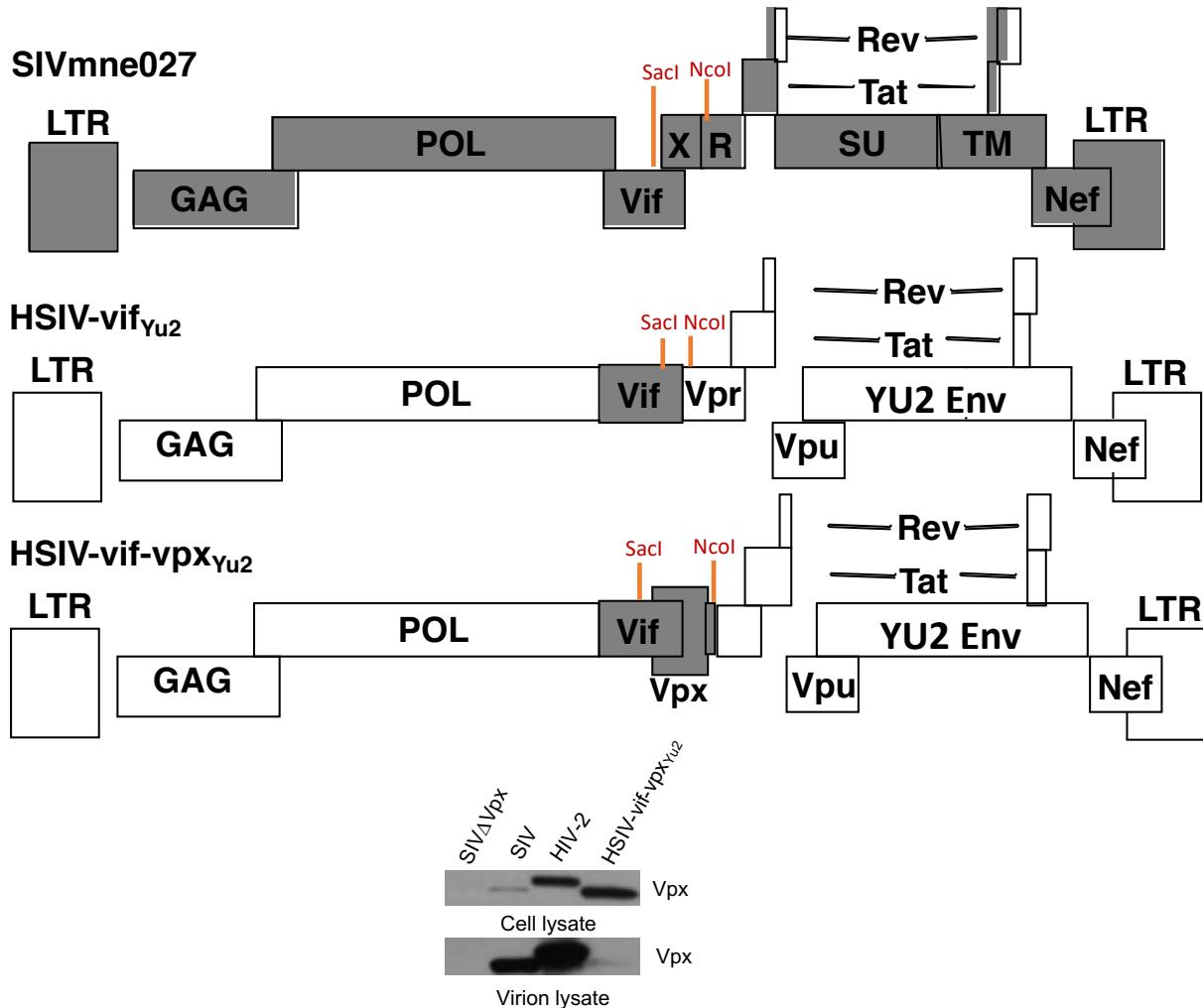


Supplementary Table 1. Synonymous mutations observed in HSIV-P3 IMCs

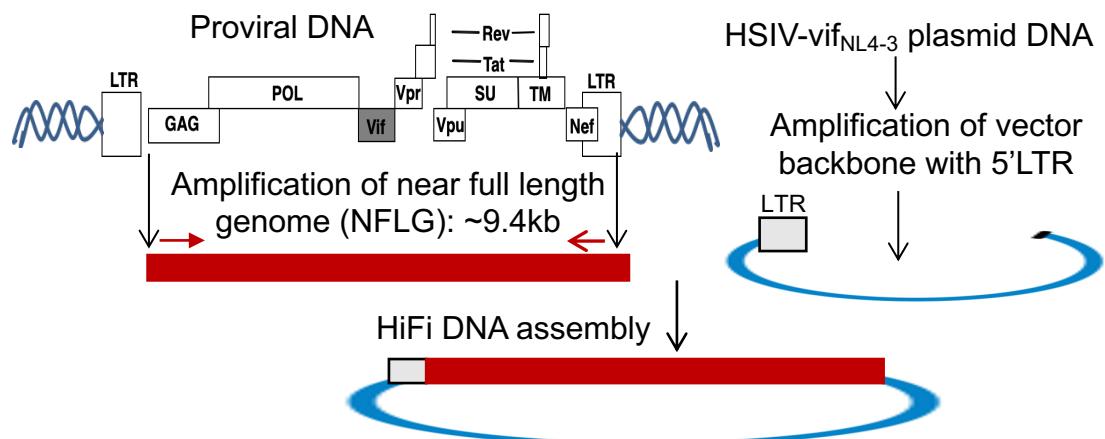
Gene	HSIV-P3-114	HSIV-P3-161	HSIV-P3-284
GAG	S9S, R58R, E208E, S234S		S9S,
POL	E184E, K508K, R999A	A78A, E184E, K508K, T627T	E184E, E379E, K508K, C780C
VIF	V10V, L109L, Q130Q	V10V, L109L, Q130Q	V10V, L109L, Q130Q
VPU	R36R, P75P		
ENV	V85V, 178K, T230T, G522G, L690L, V810V	V85V, 178K, T448T, A556A, L690L, V810V	V85V, 178K, L690L, V810V
NEF		G96G	



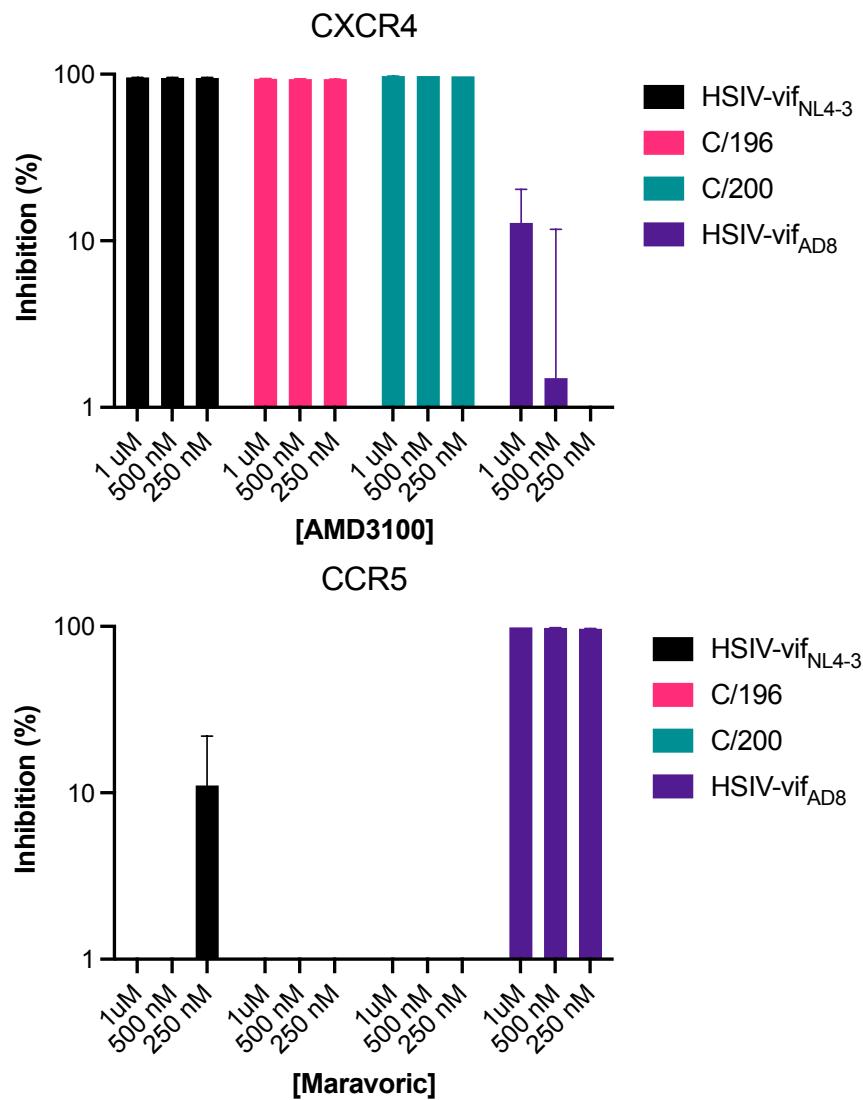
Supplementary Fig. 1: Construction of Vpr expressing HSIV-vif clones. SphI to SalI fragment of HSIV-vif_{NL4-3} encompassing HIV *gag*, *pol*, SIV *vif* and HIV-1 *vpr* genes was cloned into pCR2.1 TOPO vector. SIV *vpx* start codon and two additional ATG codons upstream of the HIV-1 *vpr* start codon were mutated by Quickchange mutagenesis and the sequence between the stop codon of *vif* and start codon of *vpr* were deleted. After mutagenesis, SphI and SalI fragment was cloned back into HSIV-vif_{NL4-3} and HSIV-vif_{AD8}. Similarly, SphI to SalI fragment of HSIV-vif_{Yu2} was cloned into pCR2.1 TOPO vector, ATG codons upstream of *vpr* were mutated, and cloned back into HSIV-vif_{Yu2}. *Approximate location of mutations introduced in the *vif* gene.



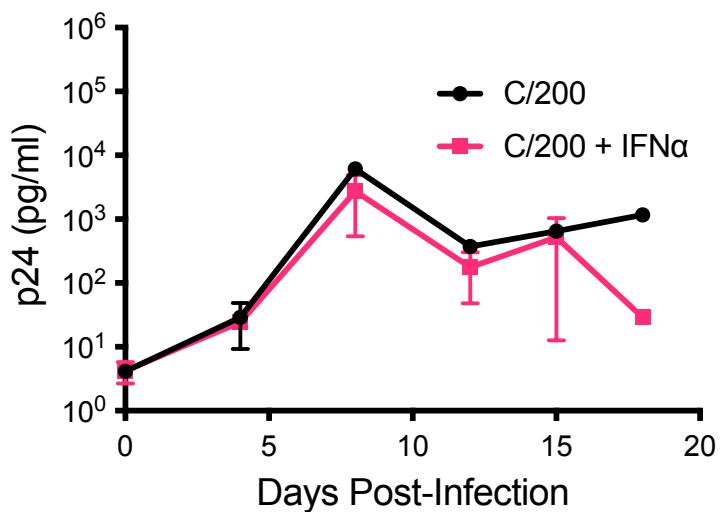
Supplementary Fig. 2: Construction of Vpx expressing HSIV-vif_{YU2}. SacI to NcoI region of HSIV-vif_{YU2} was replaced with SacI to NcoI region of SIVmne027 to generate HSIV-vif-vpx_{YU2}. 293T cells were transfected with different lentiviral plasmids. At 48 hours post-transfection, virus supernatants were collected and concentrated by centrifugation. Cell and virion lysates were analyzed by western blot using antibody to HIV-2 Vpx protein.



Supplementary Fig. 3: Schematic of HiFi DNA assembly approach to generate full length clones. Near full length genomes (NFLG) were amplified using nested PCR and cloned into a vector PCR product containing 5' LTR sequences (amplified from HSIV-vif_{NL4-3} plasmid) using NEBuilder HiFi assembly mix.



Supplementary Fig. 4: Coreceptor usage of biological clones C/196 and 200-2. TZM-bl cells were infected with different viruses in the presence of increasing concentrations of CXCR4 and CCR5 inhibitors. 48 hours later cell lysates were assayed for luciferase activity using plate based luminometer.



Supplementary Fig. 5: Replication kinetics of biological isolate of HSIV-vif_{NL4-3} (C/200). PTM CD4+ T cells were infected in duplicate at a MOI of 0.01 with C/200 in the presence or absence of IFN α (200 U/ml) in the culture media. Virus supernatants were collected every 3 to 4 dpi and p24 was quantified by ELISA.

Nef sequences:

HSIV-vif NL4-3	1	MGGKWSKSSVIGWPAVRERMR-RAEPAADGVGAVSRDLEK	39
C/196	1RA.....	40
C/200	1-Q.....	39
Acidic & PxxP			
HSIV-vif NL4-3	40	HGAITSSNTAANNAACA WLEAQEEEEVGFPVTPQVPLRPM	79
C/196	41	80
C/200	40	79
Core domain			
NHSIV-vif NL4-3	80	TYKAADVDSLHFLKEKGGLIHSQRQDILDWIYHTQG	119
C/196	81	120
C/200	80	119
C-loop			
HSIV-vif NL4-3	120	YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKG	159
C/196	121	160
C/200	120T.....	159
C-terminus			
HSIV-vif NL4-3	160	ENTSLLHPVSLHGMDDPEREV LWRFDSRLAFHHVARELH	199
C/196	161	...N.....I.....K.....	200
C/200	160	...N.....K.....Y	199
HSIV-vif NL4-3	200	PEYFKNC	206
C/196	201	207
C/200	200	206

Envelope Sequences:

HSIV-vif NL4-3	1	MRVKEKYQHLWRWGKWGTMLLGILMICSATEKLVWVTVYYGVPVWKEATTTLFCASDAKA	60
C/196	1	60
C/200	1	60
gp 120 			
HSIV-vif NL4-3	61	YDTEVHNWATHACVPTDPNPQEVVNVNTENFMWKNDMVEQMHEIDIISLWDQSLKPCV	120
C/196	61	120
C/200	61	120
V1/V2			
HSIV-vif NL4-3	121	KLTPLCVSLKCTDLKN DNTNTNSSSGRMIMEKGEIKNCNFNISTSIRDKVQKEYAFFYKLD	180
C/196	121EG.T.....K.....	180
C/200	121EG.....E.....K.....	180
HSIV-vif NL4-3	181	IVPIDNTSYRLISCNTSVIT QACPKVSFEPPIHYCAPAGFAILKCNNKTFNGTGPCTNV	240
C/196	181E.....	240
C/200	181I.....	240
V3			
HSIV-vif NL4-3	241	STVQCTHGIRPVVSTQLLNGLAEEDVVIRSANFTDNAKTIIVQLNTSVEIN CTRPNNN	300
C/196	241V.....	300
C/200	241V.....	300
301			
HSIV-vif NL4-3	301	TRKSIRIQRGPGRAFVTIGKIGNMRQAH CNISRAKWNATLKQIASKLREQFGNNKTIIFK	360
C/196	301H.....	360
C/200	301H.....	360

V4

HSIV-vif NL4-3	361	QSSGGDPEIVTHSFNCGEFFYCNSTQLFNSTWFNSTWSTEWSNNTEGSDTITLPCRIKQ	420
C/196	361M.....	420
C/200	361	420

V5

HSIV-vif NL4-3	421	FINMWQEVGKAMYAPPISGQIRCSSNITGLLTRDGNNNNNGSEIFRPGGGDMRDNRSE	480
C/196	421K.....	480
C/200	421K.....	480

gp 120 gp 41

HSIV-vif NL4-3	481	LYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLGAAGSTMGCTSMLTVQAR	540
C/196	481L.....AA.....	540
C/200	481L.....AA.....	540

HSIV-vif NL4-3	541	QLLSDIVQQQNLLRAIEAQHQHLLQLTVWGIKQLQARILAVERYLKDDQQLLGIVGCSGKL	600
C/196	541G.....	600
C/200	541G.....	600

HSIV-vif NL4-3	601	ICTTAVPWNASWSNKSLEQIWNNTWMEDREINNYTSLIHSLIEESQNQQEKNEQUELLE	660
C/196	601	660
C/200	601	660

Membrane spanning domain

HSIV-vif NL4-3	661	LDKWASLWNWFNITNWLYIKLFIMIVGGLVGLRIVFAVLSIVNVRQGYSPLSFQTHLP	720
C/196	661L.....	720
C/200	661	720

HSIV-vif NL4-3	721	IPRGPDREPREGEEGERDRDRSIRLVNGSLALIWDDLRLSCLFSYHRLRDLLLIVTRIV	780
C/196	721G.....N.....	780
C/200	721G.....	780

HSIV-vif NL4-3	781	ELLGRRGWEALKYWWNLLQYWSQELKNSAVNLLNATAIAVAEGTDRCVIEVLQAAYRAIRH	840
C/196	781I.....	840
C/200	781	840

HSIV-vif NL4-3	841	IPRRIRQGLERILL	854
C/196	841	854
C/200	841V..	854

Vif sequences:

HSIV-vif NL4-3	1	MEEEKRWIAVPTWRIPERLERWHSLIKYLKYKTKDLQRVC	40
C/196	1	40
C/200	1	40

HSIV-vif NL4-3	41	YVPHHKVGVAWWTCSRVIDPLQEESQLLEVQGYWNLTHERG	80
C/196	41	80
C/200	41E.-.	79

HSIV-vif NL4-3	81	WLSTYAVRITWYSRNFWTDVTVDYADILLHSTYFPCFTAG	120
C/196	81	120
C/200	80	119

HSIV-vif NL4-3	121	EVRAIRGEQLLSCCRFPRAHKNQVPSLQYLAIRVSYVR	160
C/196	121	160
C/200	120T.....	159

HSIV-vif NL4-3 161 SQRENPTWKQWRRDNRRSLRMAKQNSRGDKQRGSKPPTKG 200
C/196 161I..... 200
C/200 160I..... 199

HSIV-vif NL4-3 201 ADFPGLAKVLGILA 214
C/196 201 214
C/200 200 213

Supplementary Fig. 6: Sequence alignment of biological isolates (C/196 and C/200). Nef, Vif, and Envelope protein sequences of biological isolates recovered PTM MO8009 are aligned to parental HSIV-vif_{NL4-3} sequences.

Envelope sequences:

HSIV-vif _{NL4-3}	MRVKEKYQHLWRWGKWKGTMLLGILMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKA
HSIV-P3-114P.....
HSIV-P3-161
HSIV-P3-284
HSIV-vif _{NL4-3}	YDTEVHNWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCV
HSIV-P3-114Q.....R....
HSIV-P3-161Q.....R....
HSIV-P3-284Q.....R....
HSIV-vif _{NL4-3}	KLTPLCVSLKCTDLKNDTNSSSGRMIMEKGEIKNCFSNISTSIRDKVQKEYAFFYKLD
HSIV-P3-114EG.T.....K.....
HSIV-P3-161EG.T.....K.....
HSIV-P3-284EGTT.....K.....
HSIV-vif _{NL4-3}	IVPIDNTSYRLISCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNV
HSIV-P3-114E.....
HSIV-P3-161E.....
HSIV-P3-284E.....
HSIV-vif _{NL4-3}	STVQCTHGIRPVVSTQLLNGLAEDVVIRSANFTDNAKTIIVQLNTSVEINCTRPNNN
HSIV-P3-114V.....
HSIV-P3-161V.....
HSIV-P3-284V.....
HSIV-vif _{NL4-3}	TRKSIRIQRGPGRAFVTIGKIGNMRQAHNCNISRACKWNATLKQIAASKLREQFGNNKTIIFK
HSIV-P3-114H.....R.....
HSIV-P3-161H.....R.....
HSIV-P3-284H.....R.....E.....
HSIV-vif _{NL4-3}	QSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTEWSNNTEGSDTITLPCRIKQ
HSIV-P3-114M.....
HSIV-P3-161M.....
HSIV-P3-284M.....
HSIV-vif _{NL4-3}	FINMWQEVGKAMYAPPISGQIRCSSNITGLLTRDGNNNNNGSEIFRPGGDMRDNRSE
HSIV-P3-114K.....
HSIV-P3-161K.....
HSIV-P3-284K.....
HSIV-vif _{NL4-3}	LYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLGAAGSTMGAASMTLTVQAR
HSIV-P3-114L.....
HSIV-P3-161L.....
HSIV-P3-284L.....
HSIV-vif _{NL4-3}	QLLSDIVQQQNLLRAIEAQHQLLQLTVWGIKQLQARILAVERYLKDQQLGIWGCSGKL
HSIV-P3-114G.....T.....
HSIV-P3-161G.....T.....
HSIV-P3-284G.....T.....
HSIV-vif _{NL4-3}	ICTTAVPWNASWSNKSLEQIWNNTWMEDREINNYTSLIHSLIEESQNQQEKNEQELLE
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284
HSIV-vif _{NL4-3}	LDKWASLWNWFNITNWYIKLFIMIVGGLVGLRIVFAVLISIVNRVRQGYSPLSFQTHLP
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284
HSIV-vif _{NL4-3}	I PRGPDRPEGIEEGGERDRDRSIRLVNGSLALIWDDLRSICLFSYHRLRDLLLIVTRIV

HSIV-P3-114G.....N.....G
HSIV-P3-161G.....N.....G
HSIV-P3-284G.....N.....G
HSIV-vif _{NL4-3}	ELLGRRGWEALKYWWNLLQYWSQELKNSAVNLLNATAIAVAEGTDRVIEVLQAAYRAIRH
HSIV-P3-114S.....I.....
HSIV-P3-161I.....
HSIV-P3-284I.....
HSIV-vif _{NL4-3}	IPRRIRQGLERILL
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284

Nef sequences:

HSIV-vif _{NL4-3}	MGGKWSKSSVIGWPAVRERMRAEPAADGVGAVSRDLEKHGAISSNTAANNAACAWLEA
HSIV-P3-114
HSIV-P3-161T.....
HSIV-P3-284
HSIV-vif _{NL4-3}	QEEEEVGFPVTPQVPLRPMTYKAADVDSLHFLKEKGGLIHSQRQDILDLWIYHTQGY
HSIV-P3-114K.....
HSIV-P3-161K.....
HSIV-P3-284K.....
HSIV-vif _{NL4-3}	FPDWQNYTPGPGVRYPLTFWCYKLVPVEPDKEANKGENTSLLHPVSLHGMDDPEREV
HSIV-P3-114N.....I.....M
HSIV-P3-161N.....I.....
HSIV-P3-284N.....I.....
HSIV-vif _{NL4-3}	LEWRFDSRLAFHHVARELHPEYFKNC
HSIV-P3-114	...K.....D.....
HSIV-P3-161	...K.....D.....
HSIV-P3-284	...K.....D.S....

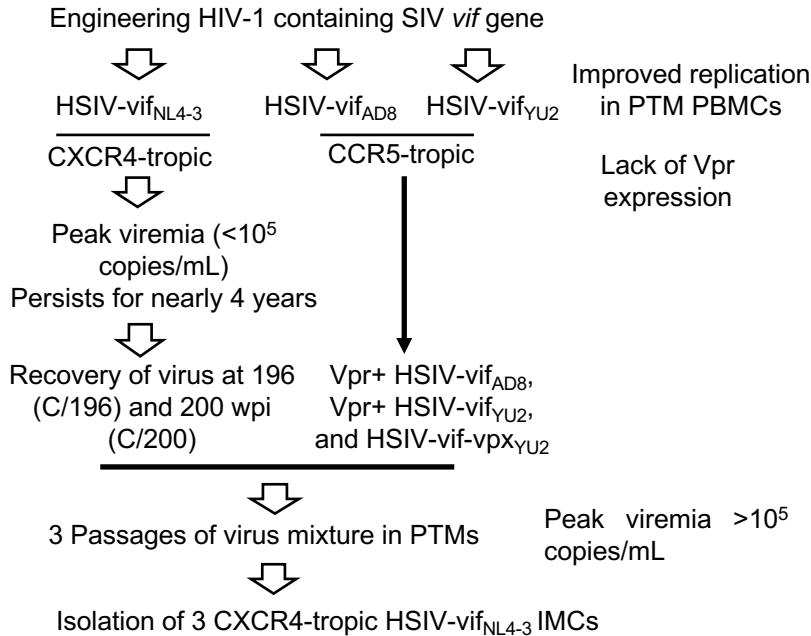
Rev Sequences:

HSIV-vif _{NL4-3}	MAGRSGDSDEELIRTVRLIKLYQSNPPNPEGTRQARRNRRWRERQRQIHSISERIL
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284
HSIV-vif _{NL4-3}	STYLGRSAEPVPLQLPPLERLTLDNEDCGTSGTQGVGSPQILVESPTVLESGTKE*
HSIV-P3-114	...E.....R.....R.....
HSIV-P3-161	...E.....R.....R.....
HSIV-P3-284	...E.....R.....R.....

Supplementary Fig. 7: Sequence alignment of HSIV-P3 IMCs. Envelope, Nef, and Rev protein sequences of HSIV-P3 IMCs are aligned to parental HSIV-vif_{NL4-3} sequences.

	Splice acceptor site
HSIV-vif _{NL4-3}	TTTACTGCATAGCACTTATTCCCT <u>TGCTTTACAGC</u> GGGAGAAGTGAGA
Vpr ⁺ HSIV clones
HSIV-P3-114A.....
HSIV-P3-161A.....
HSIV-P3-284A.....
HSIV-vif _{NL4-3}	AGGGCCATCAGGGGAGAACAACTGCTGTCTGCTGCAGGTTCCCGAGAGC
Vpr ⁺ HSIV clones
HSIV-P3-114G.....
HSIV-P3-161G.....
HSIV-P3-284G.....
HSIV-vif _{NL4-3}	TCATAAGAACCAAGGTACCAAGTCTACAGTACTTAGCACTGAGAGTAGTAA
Vpr ⁺ HSIV clones
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284
	Vpx start codon
HSIV-vif _{NL4-3}	GTT <u>ATG</u> TCAGATCCCAGAGAGAGAACCTGGAAACAGTGGAGAAGA
Vpr ⁺ HSIV clones	...ACG.....
HSIV-3-114	...ATG.....
HSIV-P3-161	...ATG.....
HSIV-P3-284	...ATG.....
	Met codon
HSIV-vif _{NL4-3}	GACAATAGGAGAACGCCTCGA <u>ATGG</u> CTAAACAGAACAGTAGAGGAGATAA
Vpr ⁺ HSIV clones <u>TTG</u>
HSIV-P3-114 <u>ATA</u>
HSIV-P3-161 <u>ATA</u>
HSIV-P3-284 <u>ATA</u>
HSIV-vif _{NL4-3}	ACAGAGAGGCAGTAACCACCTACCAAGGGAGCTGATTTCCAGGTTGG
Vpr ⁺ HSIV clones
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284
	Deletion
HSIV-vif _{NL4-3}	CAAAGGTCTTGGGAATACTGG <u>CATGAGT</u> TAGGAAACTGACAGAGGAC
Vpr ⁺ HSIV clones <u>T</u>
HSIV-P3-114 <u>T</u>
HSIV-P3-161 <u>T</u>
HSIV-P3-284 <u>T</u>
	Vpr start codon
HSIV-vif _{NL4-3}	AG <u>ATGG</u> AACAAGCCCCAGAAGACCAAGGGCC
Vpr ⁺ HSIV clones
HSIV-P3-114
HSIV-P3-161
HSIV-P3-284

Supplementary Fig. 8: Sequence alignment of SIV vif and HIV-1 vpr region of HSIV-P3 IMCs with Vpr⁺ and Vpr- HSIV-vif_{NL4-3}.



Supplementary Fig 9: Flowchart showing overall experimental plan to recover HSIV infectious molecular clones.